Amendments to the Specification:

Please amend the specification as follows:

For the paragraph spanning page 2, line 19 to page 3, line 6:

Therefore, the present inventors made the effort to carry out the following research that aims to clone novel human genes in order to solve the objectives mentioned above. First, the inventors isolated a clone comprising a full-length-enriched cDNA library that is synthesized by the oligo-capping method (Maruyama, K. and Sugano, S., Gene 138: 171-174, 1994; Suzuki, Y. et al., Gene 200: 149-156, 1997). Then, the inventors determined the nucleotide sequence of the obtained full-length-enriched cDNA clones from both 5' and 3' ends. Then, human full-length DNA, expected to be a full-length DNA by using ATGpr (Salamov, A. A. et al. Bioinfomatics 14: 384-390, 1998; ~~http://www.hri.co.jp/atgpr/~~) and so forth, was selected. By utilizing the resulting sequences of full-length-enriched cDNA clones, the inventors selected clones that were expected to contain a signal by the PSORT (Nakai, K. and Kanehisa, M. Genomics 14: 897-911 1992), and obtained clones that contain a cDNA encoding a secretory protein. The inventors have analyzed the nucleotide sequence of the full-length cDNA clones, and deduced the amino acid sequence encoded by the nucleotide sequence. Then, the inventors have performed the BLAST search (Altschul, S. F., et al. J. Mol. Biol. 215: 403-410, 1990; Gish, W., and States, D.J. Nature Genet. 3: 266-272 1993; ~~http://www.ncbi.nlm.nih.gov/BLAST/~~) of the GenBank ~~(http://www.ncbi.nlm.nih.gov/Web/GenBank/index.html)~~ and SwissProt ~~(http://www.ebi.ac.uk/ebi_docs/swissprot_db/swisshome.html)~~ using the deduced amino acid sequence.

For the paragraph spanning page 5, line 26 to page 6, line 3:

The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90: 5873-5877, 1993).Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215: 403-410, 1990). BLAST

nucleotide searches are performed with the NBLAST program, score = 100, word length = 12. BLAST protein searches are performed with the XBLAST program, score = 50, word length = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25: 3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. ~~See http://www.ncbi.nlm.nih.gov.~~

For the paragraph at page 18, lines 16 – 25.

Using the Oligo-cap linker (agcaucgagu cggccuuguu ggccuacugg/SEQ ID NO: 3) and the Oligo-dT primer (gcggctgaag acggcctatg tggccttttt ttttttttt tt/SEQ ID NO: 4), BAP (bacterial alkaline phosphatase) treatment, TAP (tobacco acid phosphatase) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme. 41: 197-201; Suzuki Y. et al. (1997) Gene 200: 149-156). Next, 5'-PCR primer (agcatcgagt cggccttgtt g/SEQ ID NO: 5) and 3'-PCR primer (gcggctgaag acggcctatg t/SEQ ID NO: 6) were used for performing PCR (polymerase chain reaction) to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pME18SFL3 was used for cloning the cDNA in an unidirectional manner, and cDNA libraries were obtained. The clones having an insert cDNA with a length of 1 kb or less were discarded. Then, the nucleotide sequence of the 5' and 3' ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM^{TM} 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BIGDYE^{TM} ~~BigDye~~ Terminator Cycle Sequencing FS Ready Reaction Kit, from by PE Biosystems) according to the instructions.

For the paragraph at page 19, lines 17 – 25.

The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation initiation codon based on the characteristics of the sequences in the vicinity of the ATG codon

[A. A. Salamov, T. Nishikawa, M. B. Swindells, Bioinformatics, 14: 384-390 (1998)~~;~~ ~~http://www.hri.co.jp/atgpr/~~]. The results are shown with expectations (also described as ATGpr1 below) that an ATG is a true initiation codon (0.05-0.94). The results indicate that the ATGpr1 value of PSEC137 was 0.94.

For the paragraph at page 22, lines 20 – 25.

As heat-resistant DNA polymerase for PCR, AMPLITAQ™ ~~AmpliTaq~~ Gold (PE Applied Biosystems) was selected to prepare the reaction solution according to the manufacturer's directions. The final concentration of the primer was 200 nM. The reaction cycle was 94°C for 10 min, followed by 40 cycles of 94°C for 30 sec, 55°C for 30 sec, and 72°C for 30 sec.